

Cancer and Artificial Agriculture: Converging Gene-Editing Toolkits, Governance, and Climate-Resilient Food Systems

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Research Article

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Posted Date: October 16th, 2026

DOI: <https://doi.org/10.21203/rs.3.rs-11373651/v1>

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Additional Declarations: The authors declare no competing interests.

CANCER AND ARTIFICIAL AGRICULTURE:
CONVERGING GENE-EDITING TOOLKITS, GOVERNANCE, AND CLIMATE-RESILIENT FOOD
SYSTEMS

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October, 2026

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ABSTRACT

Elevated atmospheric CO₂ at projected mid-century concentrations reduces iron and zinc concentrations in C3 staple crops, deepening hidden hunger in populations already dependent on those staples, while the same exposure has been reported to increase the risk of cancer and other non-communicable diseases. Responses to date remain fragmented: biofortification, offline agricultural diagnostics and gene-editing governance are studied in isolation, no framework connects climate-driven nutrient dilution to community-scale intervention, and the gene-editing toolkit and governance questions common to artificial agriculture and oncological research have not been considered together; meanwhile, centralised and cloud-dependent agritech systematically fails low-connectivity rural populations. Here we present and appraise an integrated artificial-agriculture model combining transgene-free CRISPR–Cas9 SDN-1/2 biofortification, a decentralised low-cost sensor network with an offline KNN classifier for soil and crop diagnosis, community-scale organic soil-regeneration practice, and open-access licensing under the FAO International Treaty, and we assess its evidence base through a structured synthesis of 50 peer-reviewed studies. The classifier attained author-reported precision and recall of approximately 86% across cotton, rice, wheat and zinc-fortified maize classes. Claim-by-claim appraisal rated CO₂-driven micronutrient dilution, biofortification efficacy and India's SDN-1/2 regulatory exemption as strongly supported, and product-specific performance, the reported ₹75,000 laboratory cost and the combined soil-regeneration package as weakly supported; gap analysis identified the absence of community-deployment evidence as the principal limitation. Decentralised, transgene-free artificial agriculture is therefore credible as a synthesis of proven components, but not yet as a validated, deployment-ready system, for mitigating hidden hunger and its reported oncological consequences under climate change; multi-location field trials of edited staples under elevated CO₂, leakage-resistant external validation of offline models, and comparative cost-effectiveness studies of community laboratories are the priorities this work establishes.

INTRODUCTION

1.1 Background and Rationale

Micronutrient deficiency, or "hidden hunger", persists as a widespread and worsening public-health condition. Between 2012 and 2023 the global prevalence of anaemia among women aged 15 to 49 years rose from 27.6% to 30.7%, an increase observed across nearly all regions (FAO et al., 2025), and zinc deficiency remains prevalent in populations whose food supplies depend on staple cereals (Wessells & Brown, 2012). More broadly, an estimated 2.3 billion people, 28% of the global population, were food insecure in 2024, with the burden rising in Africa and declining in Asia and Latin America (FAO et al., 2025). A further threat now acts upon the nutritional quality of the staples themselves: elevated atmospheric CO₂, at concentrations projected for mid-century, reduces iron and zinc concentrations in C3 grains and legumes under field conditions (Myers et al., 2014; Smith & Myers, 2018). Because the same exposure has been reported to increase the risk of cancer, neurological disorder, kidney

failure and bone atrophy (Blenwrith, 2017), the consequences of CO₂-driven nutrient dilution extend beyond deficiency into oncological and chronic-disease territory.

These converging pressures define the rationale for the present work. Conventional responses, centralised production, cloud-dependent agritech and patent-enclosed seed systems, systematically fail low-connectivity and low-income populations (Gumbi & Gumbi, 2023). Artificial agriculture, that is, controlled-environment, biofortified and decentralised food production, offers an alternative; and the gene-editing tools at its centre are the same tools now reshaping cancer research and therapy (Tycko et al., 2021). Yet the scientific and governance questions these tools raise, transgene-free editing, biosafety, regulatory exemption and public trust, are still debated separately in agricultural and oncological settings. This study treats them as one shared problem.

1.2 Literature Review

The evidence on CO₂-driven nutrient dilution is strong in direction but weaker in magnitude: field trials, systematic review and modelling work agree that iron and zinc decline in C3 staples under elevated CO₂ (Myers et al., 2014; Smith & Myers, 2018; Chumley & Hewlings, 2020), with reported declines of roughly 3–17% rather than a single universal figure (Smith & Myers, 2018; Raju et al., 2026), and mechanisms attributed to reduced transpiration-driven mineral delivery, carbon–mineral imbalance and impaired grain translocation (Ujiie & Ishimaru, 2019; Raju et al., 2026).

The biofortification literature describes three broad approaches. Transgene-free promoter editing has raised zinc uptake and translocation in rice without foreign DNA in progeny (Ludwig et al., 2024; Menguer et al., 2026); transgenic indica rice has attained iron and zinc dietary targets in field trials (Trijatmiko et al., 2016); and agronomic or microbial inputs have increased grain zinc and iron in context-dependent ways (Singh & Prasanna, 2020; Devkota et al., 2026). On the regulatory side, India's 2022 framework exempts SDN-1 and SDN-2 plants without foreign DNA from Rules 7–11 (Prasad, 2023; Tachikawa et al., 2024), although exemption is not equivalent to deployment readiness: biosafety, procedural and governance obligations persist (Kuzma & Grieger, 2020; Vengadesen et al., 2025). In parallel, digital-agriculture research shows that offline and edge-based designs outperform cloud-first systems in connectivity-constrained settings (Gumbi & Gumbi, 2023; Manjunath et al., 2026), and that machine-learning soil-nutrient prediction can be accurate locally (Acir, 2025; Chambers, 2021; Sharma et al., 2025) but degrades across locations and is vulnerable to data-leakage inflation under non-spatial cross-validation (Hengl et al., 2017; John et al., 2025).

Taken together, this literature remains fragmented. Evidence syntheses identify no study linking climate-driven nutrient dilution to community-scale intervention workflows, and governance research on locally controlled deployment is thin (Ajates & Bocci, 2025; Frison, 2018). Nor has the convergence between the gene-editing toolkit of artificial agriculture and that of oncology been examined as a single object of study. There is therefore a need for an

integrated treatment that appraises both the components and the assembled evidence base of such a system.

1.3 Conceptual Frameworks and Study Aims

This study addresses the above gap by examining artificial agriculture as an integrated system and appraising its claims against the published evidence. The conceptual framework rests on three pillars. First, 'convergent toolkits': CRISPR–Cas9 and related editing platforms, and the governance debates surrounding them, are common to crop biofortification and to cancer research, so lessons on transgene-free design and regulatory exemption transfer between the two fields (Ludwig et al., 2024; Prasad, 2023; Tycko et al., 2021). Second, 'decentralised intelligence': low-cost sensor networks and offline machine learning place diagnosis and prediction inside the communities they serve (Gumbi & Gumbi, 2023; Manjunath et al., 2026). Third, 'open governance': licensing under the FAO International Treaty on Plant Genetic Resources for Food and Agriculture avoids patent lock-up and supports farmers' seed rights (Ajates & Bocci, 2025; Frison, 2018).

The goal of this research is to present this integrated model, transgene-free SDN-1/2 biofortification within a controlled-environment module, a decentralised sensor network with KNN-based classification, community-scale soil-regeneration practice, and open-access licensing, and to appraise its evidence base through a structured synthesis of the peer-reviewed literature. In doing so, the work seeks to separate what is already supported from what remains to be validated, and to set out the priority research questions for the field.

METHODS

2.1 Overview of System Design

The system under study is a decentralised, controlled-environment production module designed for community-scale deployment (Figure 1). The module integrates multi-layer plant racks with an aquaponics loop, a filtration tank, cooling vents, and a geomembrane envelope with double-bubble insulation and anti-pest mesh to stabilise the growing environment. Instrumentation comprises a CO₂ sensor, combined NPK and pH probes, and a temperature probe; together with pre-analysed site data, these feed a local acquisition layer that supplies the classification and recommendation models described in Section 2.4. The design premise follows the digital-agriculture literature: in connectivity-constrained settings, offline and edge-based architectures outperform cloud-first systems (Gumbi & Gumbi, 2023; Manjunath et al., 2026), and all sensing, prediction and recommendation functions are therefore specified to operate without continuous cloud access.

2.2 Transgene-Free Genome-Editing Protocol

To counter CO₂-driven dilution of iron and zinc, the production protocol applies targeted CRISPR–Cas9 editing under SDN-1 and SDN-2 protocols to up-regulate the plant's native ZIP and NRAMP transporter gene families. The molecular approach disables genomic

repressors and optimises native promoter regions so as to raise root mineral uptake without inserting foreign DNA; in parallel, a CRISPR-activation (CRISPRa) configuration, a catalytically dead Cas9 fused to the VP64 activation domain, is specified to amplify transcription at target loci without double-strand cleavage, avoiding the metabolic overload and yield drag associated with constitutive over-expression. Because no foreign DNA is retained, the protocol is designed to fall within the exemption that places SDN-1/2 products outside Rules 7–11 of India's GMO framework (Prasad, 2023; Tachikawa et al., 2024), while recognising that exemption does not remove continuing biosafety and procedural obligations (Kuzma & Grieger, 2020; Vengadesen et al., 2025). Alignment with fast-track, non-GMO regulatory pipelines and with the Indian Government's C20 mandate for rapid, scalable food security is an explicit design requirement.

2.3 Soil-Regeneration Protocol

The module's substrate is produced through a staged fermentation and amendment protocol (Appendix A). In brief, a nutrient broth is prepared from animal bone (fish, goat or bone marrow) and combined in an earthen or iron vessel with cow dung, cow urine and approximately 20 L of water. To this are added 2 kg of crushed jaggery as the sugar source, 2 kg of sprouted black gram as the nitrogen and enzyme source, 2 kg of neem-oil cake for nutrients and pest control, and 2 L each of milk and buttermilk to inoculate lactic-acid bacteria; the mixture ferments covered, in a warm and dark place, for 15 to 21 days with daily stirring. The mature ferment is then combined with a solid base of two to three parts topsoil to one part organic compost or vermicompost, one part crushed charcoal (biochar) as a "terra preta"-type amendment for nutrient retention and microbial habitat, and diverse green leaves (neem, mango or guava) as organic matter, following the San Cai framing; the liquid ferment is diluted 1:10 to 1:20 and applied as a soil drench or foliar spray. Each amendment class corresponds to interventions with preliminary field support (Singh & Prasanna, 2020; Thakur et al., 2025; Xu et al., 2023), although site-specificity of biochar effects is recognised (Rodríguez-Vila et al., 2022).

2.4 Data Collection and the KNN Classification Model

Environmental and substrate data from the sensor layer are combined with pre-analysed site data and farmer inputs to form the feature set for a k-nearest-neighbour (KNN) classifier that issues hyper-localised soil and crop recommendations. Soil-type structure is visualised by principal-component analysis (Figure 2). The classifier is trained on labelled examples spanning four crop classes, cotton, rice, wheat and zinc-fortified maize, and implemented in a hosted Python notebook environment (Google Colab). Evaluation is performed on a held-out test set: precision, recall and F1 score are reported per crop class, together with actual-versus-predicted crop-class counts. In light of documented risks of validation inflation through data leakage in soil-nutrient modelling (Hengl et al., 2017; John et al., 2025), test-set separation is treated as the minimum reporting standard here, and leakage-resistant external validation is designated as future work (Chapter 4).

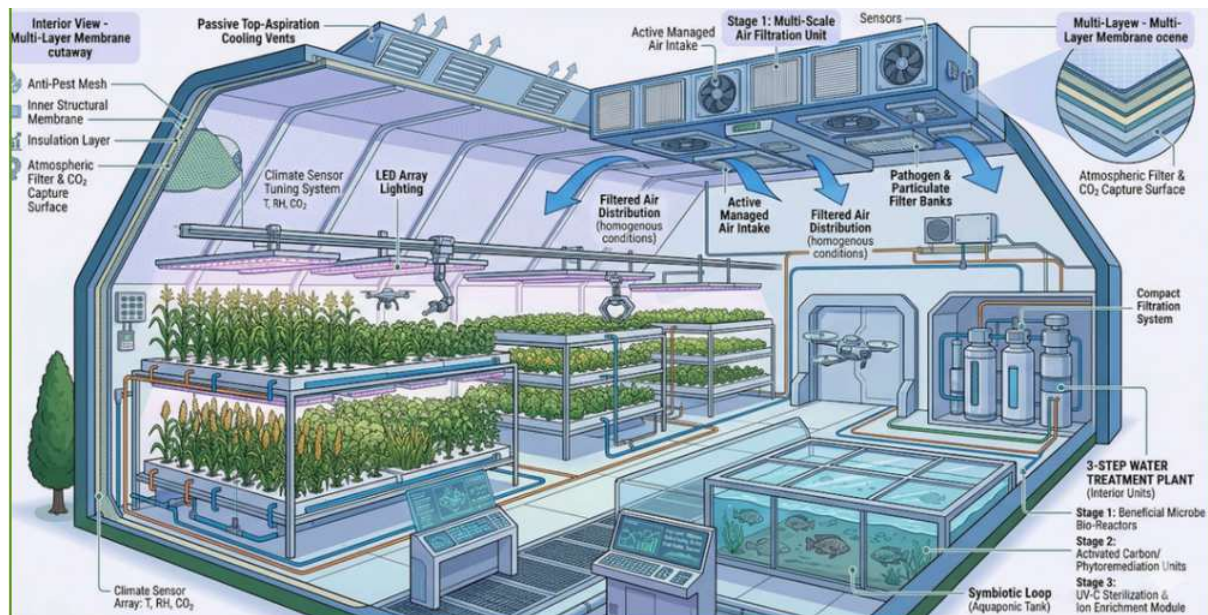
2.5 Evidence-Synthesis Procedure

To appraise the evidence base of the integrated model, a structured literature synthesis was conducted using the Consensus platform, which searches more than 220 million papers indexed from Semantic Scholar, PubMed and other scholarly sources. Twenty topic searches and one citation-graph use retrieved 532,400 records; after de-duplication and relevance and quality screening, 627 papers were eligible, and the top 50 were included in the final analysis. Searches targeted six linked claim clusters: CO₂-driven nutrient dilution; hidden-hunger economics; offline soil prediction; decentralised diagnostics; transgene-free CRISPR editing; and seed governance and access. Included claims were graded as strongly or weakly supported according to the directness and consistency of the underlying evidence; the appraisal is reported in Chapter 3.

2.6 Evaluation Framework and Analysis

Finally, the integrated model was evaluated against three alternative deployment archetypes, centralised transgenic programmes, corporate enterprise platforms, and cloud-dependent agritech, across seven criteria: capital expenditure; genetic and bioengineering approach; regulatory velocity and market access; biosafety and biosecurity; value-chain fragility; nutritional rescue capacity; and soil and microbiome integration (Table 1). Analysis is descriptive and comparative: model metrics are reported per crop class, claim-level evidence gradings are tabulated, and the four archetypes are assessed criterion by criterion. No inferential claims are made beyond those supported by the underlying sources.

Figures, Tables and Appendix used in this Chapter:



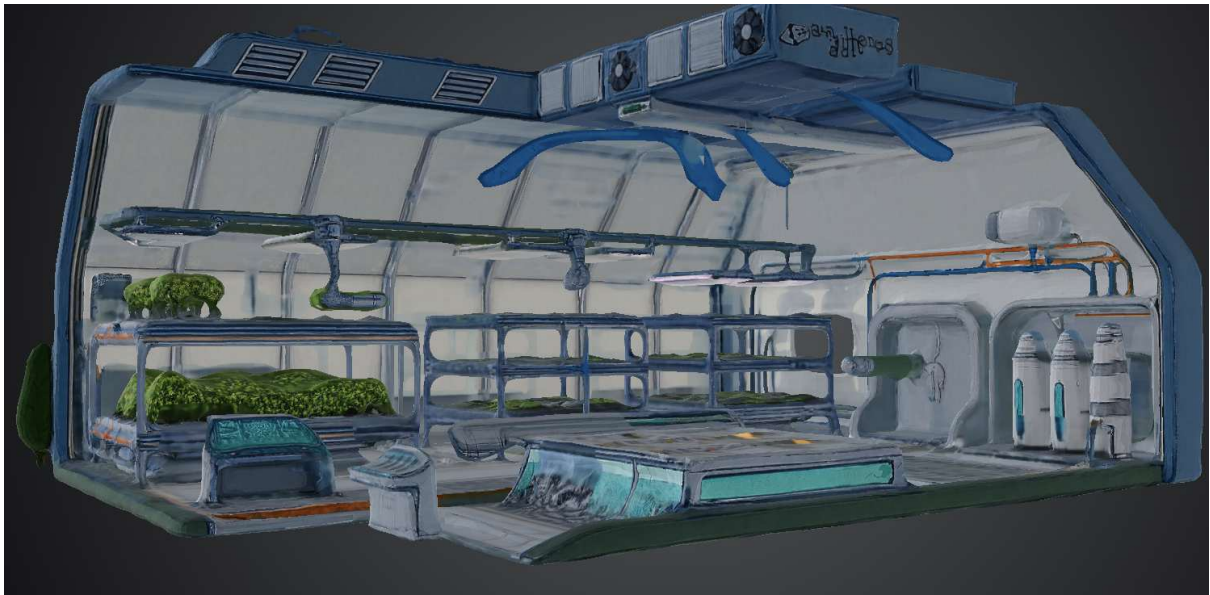


Figure 1. Controlled-environment module schematic (greenhouse with plant racks, aquaponics, filtration, vents, geomembrane).

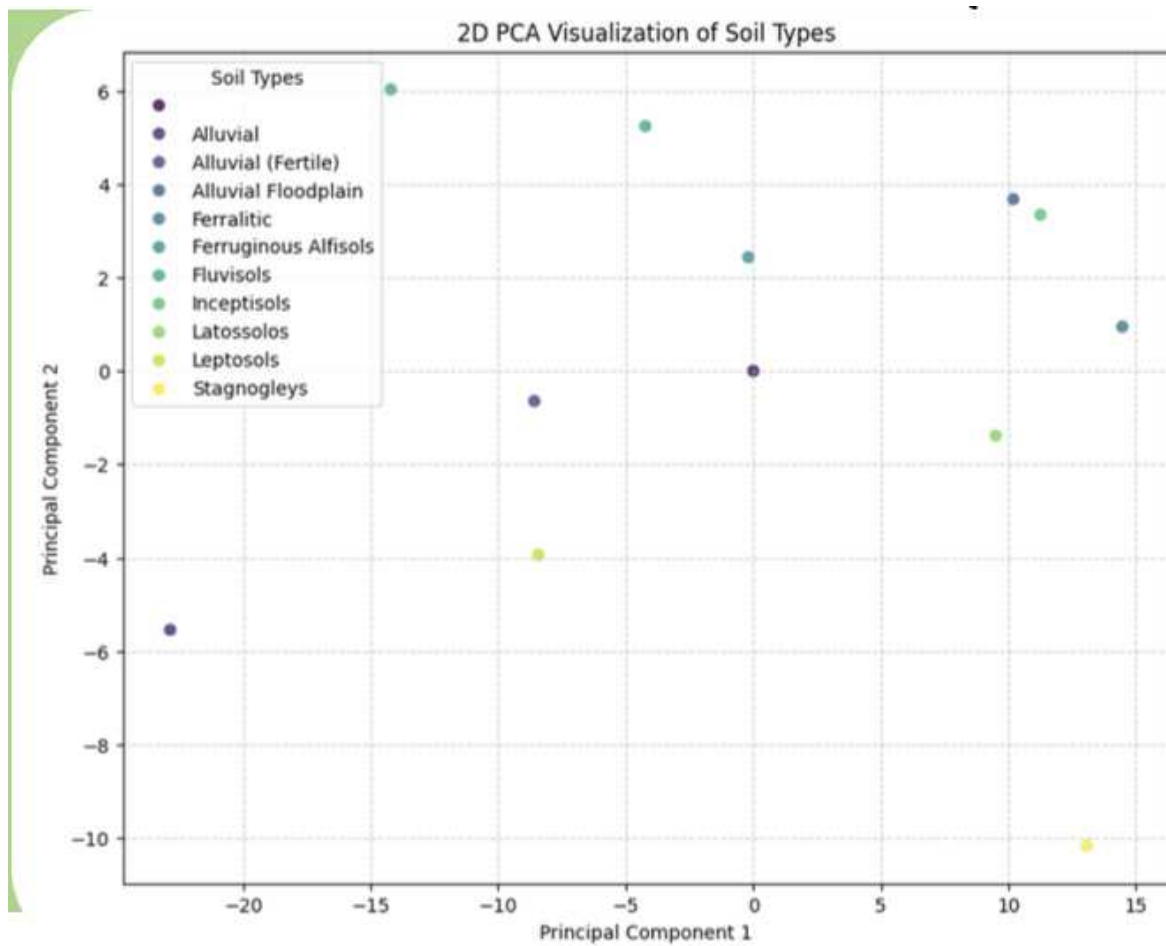
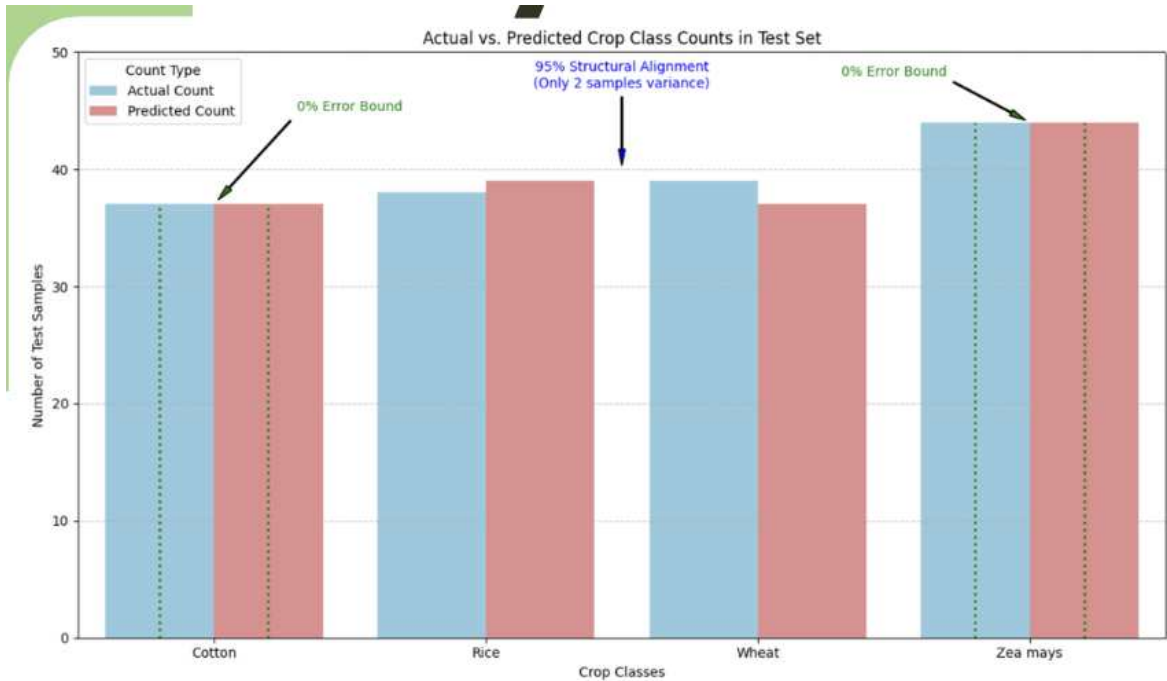


Figure 2. 2-D PCA visualisation of soil types



Source:kNN Model

Table 1. Evaluation matrix: four deployment archetypes × seven criteria

Sustainable Societies require Sustainable Solutions

To combat the climate-driven Carbon Dilution Effect—which causes a 17.5% collapse in vital nutrients like zinc (Zn) and iron (Fe) in staple crops under elevated CO2 levels—CRC Global utilizes targeted CRISPR-Cas9 (SDN-1/2) genome editing to permanently up-regulate the plant's native ZIP and NRAMP transporter gene families. Operating under transgene-free SDN-1 and SDN-2 protocols, our molecular approach carefully disables genomic repressors and optimizes native promoter regions to transform the crop's roots into high-efficiency mineral pumps without inserting any foreign DNA. Furthermore, our architecture is future-proofed with CRISPR Activation (CRISPRa), deploying a non-cleaving Dead Cas9 (dCas9) fused to a compact VP64 activation domain to dynamically amplify transcription while entirely bypassing metabolic overload and yield drag. This precise biomolecular intervention introduces zero foreign transgenes, allowing it to seamlessly align with fast-tracked, non-GMO regulatory pipelines and the Indian Government's C20 mandates for rapid, scalable global food security.

1.LabXchange. (n.d.). Introduction to genome editing with CRISPR-Cas9 [Online simulation]. Harvard University. https://www.labxchange.org/library/pathway/lx-pathway/bb8452c8-ab9c-436d-b734-b4438f2bbe10/items/b1abXchange:3c33435dix_simulation/1/56419?source=%2Flibrary%2Fclusters%2Fcluster%3A1xc-crispr-hiv&fullscreen=true

2.Tycko, J, Hess, G. T., Jeng, E. E., Dubreuil, M., & Bassik, M. C. (2017). The expanding CRISPR toolbox [Poster]. Nature Methods. https://media.nature.com/full/nature-cms/uploads/ckeditor/attachments/7742/CRISPR_poster-WEB.pdf [1, 2]

- 1.Boil animal waste (fish, goat, or bone marrow) in water until it forms a rich broth.
2. In a large earthen or iron pot, combine the broth with 15–20kg of cow dung, 15–20L of cow urine, and 20L of water.
- 3.Stir in 2kg of crushed jaggery (sugar source), 2kg of sprouted black gram (nitrogen/enzymes), 2kg of neem oil cake (nutrients/pest control), and 1L each of milk and buttermilk (lactic acid bacteria).
4. Cover and keep in a warm, dark place for 15 to 21 days. Stir the mixture once every day.
- 5.Combine 2 to 3 parts topsoil with 1 part organic compost or vermicompost.
- 6.Mix in 1 part crushed charcoal (biochar). This is the "Terra Preta" element that holds nutrients and provides a home for microbes.
7. Mix in a handful of neem manure and finely chopped green leaves (neem, mango, or guava) to provide diverse organic matter (San Cai principle).
- 8.Once the liquid fermentation (Step 1) is mature, take 1 part of the liquid and dilute it with 10 to 20 parts water.
9. Pour the diluted liquid over your solid base until it is damp but not waterlogged.
- 10.Use this enriched soil mix directly in your planting beds, or apply the diluted liquid as a foliar spray or soil drench around existing plants.

Appendix A. Full step-by-step fermentation/amendment protocol

RESULTS

3.1 Classification Performance

The KNN classifier attained author-reported aggregate precision of 86.2% and recall of 86.3% on the held-out test set. Performance varied by crop class (Figure 3, Table 2): rice achieved the highest scores, with recall near 0.95, followed by zinc-fortified maize; cotton and wheat recorded the lowest per-class metrics, with F1 scores in the approximate range 0.76–0.83. Predicted crop-class counts tracked actual counts closely across all four classes in the test set (Figure 4); the source figure annotates per-class error bounds and a KNN centroid-consistency measure, the exact values of which are to be confirmed against the model log. In the feature space, the nine soil-type classes occupied largely distinct regions of the first two principal components, with limited overlap between adjacent types (Figure 2), supporting the separability assumption on which the nearest-neighbour decision rule relies.

3.2 Claim-Level Evidence Appraisal

The structured synthesis graded the model's central claims into two tiers (Table 3). Three claims were graded "strongly supported": that elevated CO₂ reduces iron and zinc in many C3 staples, on replicated field, review and modelling evidence (Myers et al., 2014; Smith & Myers, 2018; Raju et al., 2026); that biofortification can improve iron and zinc in staples, including field rice data (Devkota et al., 2026; Stangoulis & Knez, 2022; Trijatmiko et al., 2016); and that India permits some transgene-free SDN-1/2 crops outside the GMO rules, on clear policy language that nonetheless retains procedural conditions (Prasad, 2023; Tachikawa et al., 2024; Vengadesen et al., 2025). Two claims were graded "weakly supported": that the offline model and the low-cost laboratory are already validated, the corpus supports analogous tools rather than this specific system's performance (Balkrishna et al., 2025; Lok et al., 2026), and that the combined Vrikshayurveda, San Cai and terra-preta package reliably regenerates micronutrient systems, for which support is early, fragmented and strongly site-dependent (Rodríguez-Vila et al., 2022; Thakur et al., 2025; Xu et al., 2023).

Two headline quantities additionally required calibration against the literature. The documented CO₂-driven decline spans approximately 3–17% depending on crop and condition, rather than a single universal 17.5% figure (Smith & Myers, 2018), and the strongest economic estimates place average GDP losses from micronutrient malnutrition near 1%, with India-specific short-term costs of 0.8–2.5%, rather than a 5%-of-GDP framing (Stein et al., 2007).

3.3 Comparative Assessment of Deployment Archetypes

Assessed against the seven criteria of Table 1, the community model differentiated itself most sharply on capital structure, regulatory pathway and nutritional focus. On capital expenditure it is specified at a fixed, author-reported ₹75,346 per module, against ultra-high capital expenditure for centralised transgenic programmes, high-cost enterprise laboratories for the corporate archetype, and low-upfront-but-recurring pricing for cloud-dependent agritech. On genetic and bioengineering approach it is the only archetype combining transgene-free SDN-1/2 CRISPR editing with local deployment; the corporate and cloud archetypes offer

diagnostics-only hardware or data-and-advisory platforms with no editing capability. On regulatory velocity and market access, avoiding the transgenic trigger yields the fastest robust pathway, against eight-to-ten-year approval timelines for transgenics. On biosafety and biosecurity the model is built around the components identified in the GAO (2026) comparison, whereas the cloud archetype carries no physical biosafety layer. On value-chain fragility, offline decentralised operation contrasts with high vulnerability to centralised infrastructure and with cloud systems' failure in low-connectivity settings. On nutritional rescue capacity, the model targets zinc and iron loss directly, whereas yield-and-pest programmes prioritise tonnage, corporate diagnostics cannot prove crop nutrition, and cloud platforms have no capability to address nutrient decline. On soil and microbiome integration, the model combines precision soil data with biological amendment, against synthetic-input dependence, limited soil metrics, or satellite mapping that misses local soil conditions.

3.4 Economic and Access Outcomes

The commercial design is business-to-business and business-to-government (B2B/B2G). The facility is specified as a high-return, localised installation intended to guarantee regional food sovereignty, integrating premium hardware, including an RS485 7-in-1 soil probe for precision data collection and UV-C sterilisation systems to maintain regional seed purity, while being priced to meet the international biosecurity requirements highlighted in the February 2026 GAO report, with built-in protocol monitoring and safe genetic distribution at a fraction of the cost of commercial facilities (GAO, 2026). Rather than enclosing the technology behind corporate patents, which would price out the populations that need it most, the model operates on an open-access basis under the FAO International Treaty on Plant Genetic Resources for Food and Agriculture, framing seed and protocol access as a commons (Frison, 2018).

Figures, Tables and Appendix used in this Chapter:

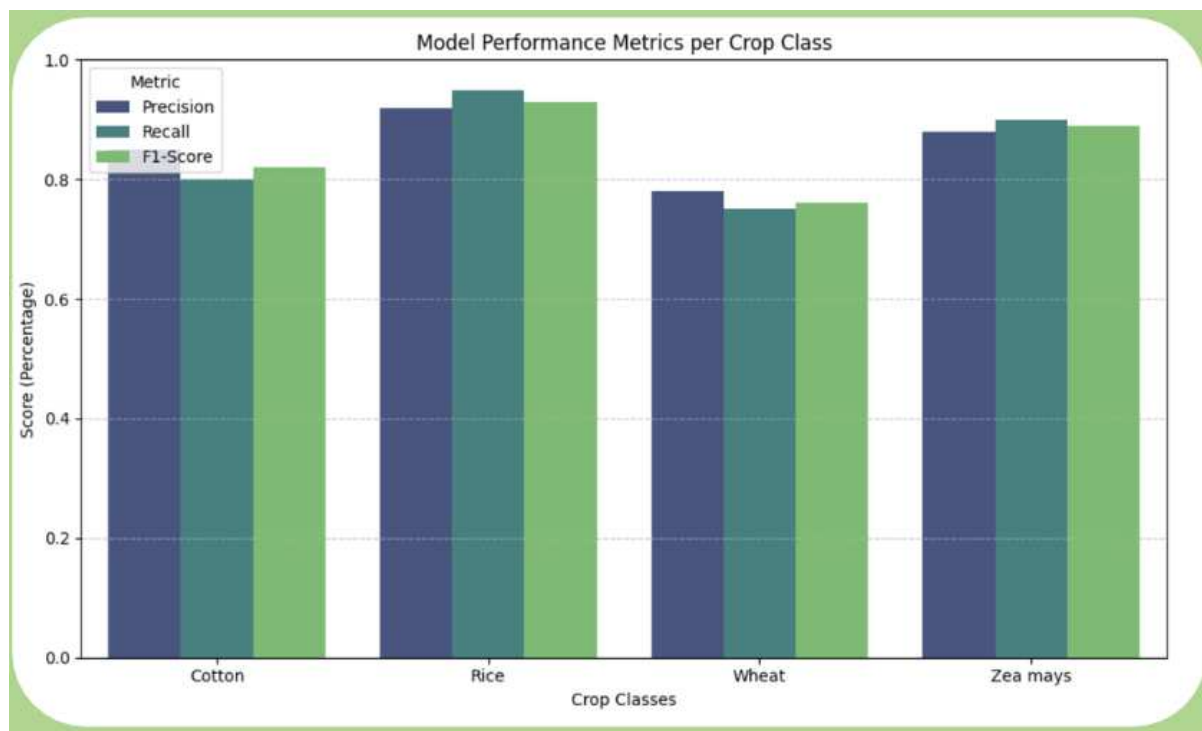


Figure 3. Model performance metrics per crop class

Crop Class	Precision	Recall	F1 Score
Cotton	≈0.80	≈0.80	≈0.83
Rice	≈0.91	≈0.95	≈0.92
Wheat	≈0.78	≈0.76	≈0.76
Zinc Maize	≈0.88	≈0.90	≈0.88

Table 2. Per-crop-class performance of the KNN classifier

Claim	Grade	Basis
Elevated CO2 reduces Fe/Zn in many C3 staples	Strong	Replicated field, review and modelling evidence
Biofortification can improve Fe/Zn in staples	Strong	Multi-approach support, including field rice data
India allows some transgene-free SDN1-2 crops outside GMO rules	Strong	Clear policy language, with continuing procedural conditions
The offline model and low-cost lab are already validated	Weak	Corpus supports analogous tools, not system-specific performance
Vrikshayurveda + San Cai + terra preta reliably regenerate micronutrient systems	Weak	Early and fragmented support; strong site dependence

Table 3. Claim-level evidence appraisal

DISCUSSION & PERSPECTIVES

4.1 Overview

This study set out to present an integrated artificial-agriculture model, transgene-free SDN-1/2 biofortification within a controlled-environment module, decentralised offline sensing with KNN-based classification, community-scale soil regeneration, and open-access licensing, and to appraise its evidence base. The principal finding is that the model is credible as a synthesis of proven components but not yet as a validated, deployment-ready system: the climate–nutrition threat, biofortification efficacy, and India's regulatory exemption pathway are strongly supported in the literature, whereas the system's own performance metrics, cost claim, and integrated soil-regeneration package are not. This chapter interprets the convergence between the gene-editing toolkits of agriculture and oncology, calibrates the gap between enthusiasm and validation, draws out governance and biosecurity implications, and states the study's limitations.

4.2 The Convergent Toolkit: What Transfers Between Agriculture and Oncology

The central observation of this work is that the same molecular toolkit, CRISPR–Cas9 nucleases and catalytically dead dCas9 effectors such as VP64-based CRISPR activation, now underwrites both crop editing and oncological research (Tycko et al., 2021). What transfers between the two fields, on the evidence assembled here, is not any product but a governance problem-set: how to regulate editing outcomes rather than process markers, and how to preserve biosafety oversight and public trust while exemptions accelerate development (Kuzma & Grieger, 2020; Prasad, 2023; Saini et al., 2026; Vengadesen et al., 2025). Agriculture's earlier experience with this toolkit supplies a cautionary precedent for every later-adopting field: exemption is not deployment, and technical feasibility has repeatedly outrun field performance and nutritional-outcome evidence (Ludwig et al., 2024). The two fields also meet at the level of environmental exposure: the same elevated CO₂ that dilutes staple micronutrients has been reported to increase oncological and chronic-disease risk (Blenwrith, 2017), so interventions that stabilise grain micronutrient density address the deficiency burden and, at least in principle, one reported contributory pathway. What does not transfer should be stated with equal clarity: the SDN-1/2 exemption is a product-class device tied to the absence of foreign DNA under a specific national instrument (Rules 7–11), and the synthesis identified no oncological analogue; cross-domain regulatory transfer therefore remains a proposition of this study, not a demonstrated result.

4.3 Calibrating Claims: Enthusiasm Versus Validation

The appraisal pattern, strong components, weak integration, mirrors the maturity of the underlying literature, in which deployment-oriented evidence is concentrated after 2020 and long-term field validation remains thin. The gap analysis makes the imbalance precise: CO₂ nutrient-dilution research defines the risk but stops at broad mitigation categories, with no

studies testing a full local-response pipeline; genome-editing studies demonstrate trait feasibility but lack multi-location field performance and human nutritional outcomes; and no studies at all link climate-driven nutrient dilution to community-scale intervention workflows. A second structural gap lies in governance: the International Treaty supports access and benefit-sharing for breeding materials, but open access does not by itself resolve breeder-skill bottlenecks, commercialisation conditions, or farmers' long-term autonomy (Ajates & Bocci, 2025; Frison, 2018). The claim that the community model "removes corporate dependencies" is therefore stronger than the current governance evidence. Quantitative calibration points in the same direction: documented micronutrient declines span roughly 3–17% rather than a single 17.5% figure, and the strongest economic estimates approach 1% of GDP on average, with India-specific short-term costs of 0.8–2.5%, rather than a 5% framing (Smith & Myers, 2018; Stein et al., 2007).

4.4 Governance, Access and Biosecurity Implications

Three implications follow for policy. First, regulation of edited crops is moving toward principle-based frameworks in which the presence or absence of foreign DNA, rather than the editing method per se, determines oversight intensity (Vengadesen et al., 2025); the model's transgene-free design is positioned for this regime, but risk assessment, transparency and public-trust work remain live obligations even where exemptions exist (Kuzma & Grieger, 2020; Saini et al., 2026). Second, community-led governance models are emerging as the complement to technical capability, and the present design's open-access licensing under the FAO Treaty, deliberately chosen over patent enclosure, which prices out the populations most in need, aligns with that direction (Frison, 2018). Third, at the level of biosecurity, the model's procedural monitoring and safe genetic-distribution provisions track the components identified in the GAO (2026) comparison of G20 members, and its open-access route avoids the multi-million-dollar regulatory costs that otherwise concentrate edited-seed capability in a few corporate actors; the people–planet–profit framing of the original proposal is, in academic register, an argument that scientific, ecological and financial viability must be designed as a single loop rather than traded off.

4.5 Limitations and Future Research

Several limitations qualify these conclusions. Model evaluation is internal and author-reported: a single held-out test set without leakage-resistant external validation, against documented risks of validation inflation in soil-nutrient modelling (Hengl et al., 2017; John et al., 2025). The evidence synthesis rests on one platform's corpus of 50 included papers, so claim gradings are corpus-dependent. The soil-regeneration package draws on early, site-dependent evidence, with biochar effects variable across soils and the San Cai element present in the literature mainly as historical framing rather than validated intervention (Rodríguez-Vila et al., 2022; Thakur et al., 2025; Xu et al., 2023). The oncological linkage is conceptual, resting on a single working-paper exposure claim and on toolkit commonality; no oncological empirical data appear in the corpus. Economic figures, including the per-module cost, remain unverified outside the proposal.

Future research should therefore prioritise: multi-location field trials testing whether transgene-free SDN-1/2 edits maintain higher grain zinc and iron under elevated CO₂; leakage-resistant external validation of offline soil-stress and nutrient-dilution models across villages; and comparative cost-effectiveness studies of village-scale bioformulation and diagnostic laboratories against centralised services. Governance studies of locally controlled deployment, addressing breeder skill, commercialisation conditions and farmer autonomy, form the necessary fourth strand.

Chapter 5: Conclusions

This study set out to present an integrated artificial-agriculture model and to appraise its evidence base against the peer-reviewed literature, treating the gene-editing toolkits of agriculture and oncology, and the governance questions they share, as a single object of study. The appraisal returns a deliberately two-sided answer. The model's problem statement and components stand on strong ground: elevated CO₂ reduces iron and zinc in C3 staples under field conditions; biofortification, including transgene-free editing, can restore those nutrients; and India's SDN-1/2 exemption provides a lawful pathway for transgene-free products outside the GMO rules. The integration-level claims do not yet stand at the same level: system-specific performance, per-module cost and the combined soil-regeneration package remain supported only by analogous tools and by early, site-dependent evidence. The honest position of this work is therefore that decentralised, transgene-free artificial agriculture is a promising synthesis of proven parts, not yet a validated, deployment-ready whole.

Within that boundary, the study makes four contributions. First, a complete system specification, controlled-environment production, transgene-free SDN-1/2 editing with CRISPRa amplification, offline sensing with KNN-based classification, community-scale soil regeneration, and open-access licensing under the FAO Treaty, assembled in a single evaluable frame. Second, a claim-level evidence appraisal that separates what is supported from what is asserted, including calibration of two headline quantities (the micronutrient decline and the GDP loss) to the ranges the literature actually sustains. Third, an articulation of the convergence between crop editing and oncological research: a shared molecular toolkit and a shared governance problem-set, together with an explicit statement of where the analogy stops. Fourth, a criterion-by-criterion comparison against centralised transgenic, corporate and cloud-dependent archetypes, in which the community model differentiates itself on capital structure, regulatory pathway, biosecurity posture and nutritional rescue capacity. Taken together, these contributions restate, in academic register, the proposal's people–planet–profit argument: scientific, ecological and financial viability are designed as one loop, not traded off against one another.

Multi-location field trials must test whether transgene-free edits hold grain zinc and iron under elevated CO₂; offline models require leakage-resistant external validation across

villages; village-scale laboratories require comparative cost-effectiveness evidence against centralised services; and locally controlled deployment requires governance research on breeder skill, commercialisation conditions and farmer autonomy. Hidden hunger and the reported oncological burden of a changing atmosphere are not, on the evidence assembled here, separate problems; and a society that would address them must do so with calibrated claims, open governance, and tools validated in the communities they serve. Sustainable societies require sustainable solutions; the burden of this work has been to distinguish, within that slogan, what is already proven from what must still be shown.

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